Amendments to the Specification:

Please insert the following new paragraph after the title on page 1:

This application is a 35 U.S.C. § 371 National Stage filing of PCT/US00/30294, filed on November 2, 2000, which claims the benefit under 35 U.S.C. § 119(e) of United States Provisional Application No. 60/163,132, filed on November 2, 1999.

Please replace the paragraph beginning at line 42 on page 35 with the following replacement paragraph:

Table 2 shows the VEGF variant identifier name, the amino acid substitutions introduced, and the codon encoding the respective substituted amino acids. The asterisk (*) next to certain variant identifiers (such as LK-VRB-1s) indicates various VEGF variants which demonstrated particularly preferred binding affinities and/or biological activities. The variant identifiers which contain an "s" (such as LK-VRB-1s) indicate VEGF variant polypeptides which consisted of the 1-109 truncated form of VEGF and contained the recited mutations provided in the Table. The variant identifiers which contain an "f" (such as LK-VRB-1f) indicate VEGF variant polypeptides which consisted of the full length 1-165 form of VEGF (amino acid residues 27-191 of SEQ ID NO:4) and contained the recited mutations provided in the Table. The $VEGF_{165}$ was encoded by the nucleotide sequence of SEQ ID NO:3. The naming and identification of the mutations in the variant sequences is in accord with naming convention. For example, for the first entry in Table 2, the mutation is referred to as "M18E". This means that the 18 position of the native VEGF sequence (using the numbering in the amino acid sequence for native human VEGF as reported in Leung *et al., supra* and Houck *et al., supra*) was mutated so that the native methionine (M) at that position was substituted with a glutamic acid (E) residue to prepare the VEGF variant. The column in Table 2 referred to as "Nucleotide Sequence" provides the respective codons coding (5' → 3') for each of the respective amino acid mutations. For example, for the first entry in Table 2, the M18E mutation is coded by the codon "GAG."